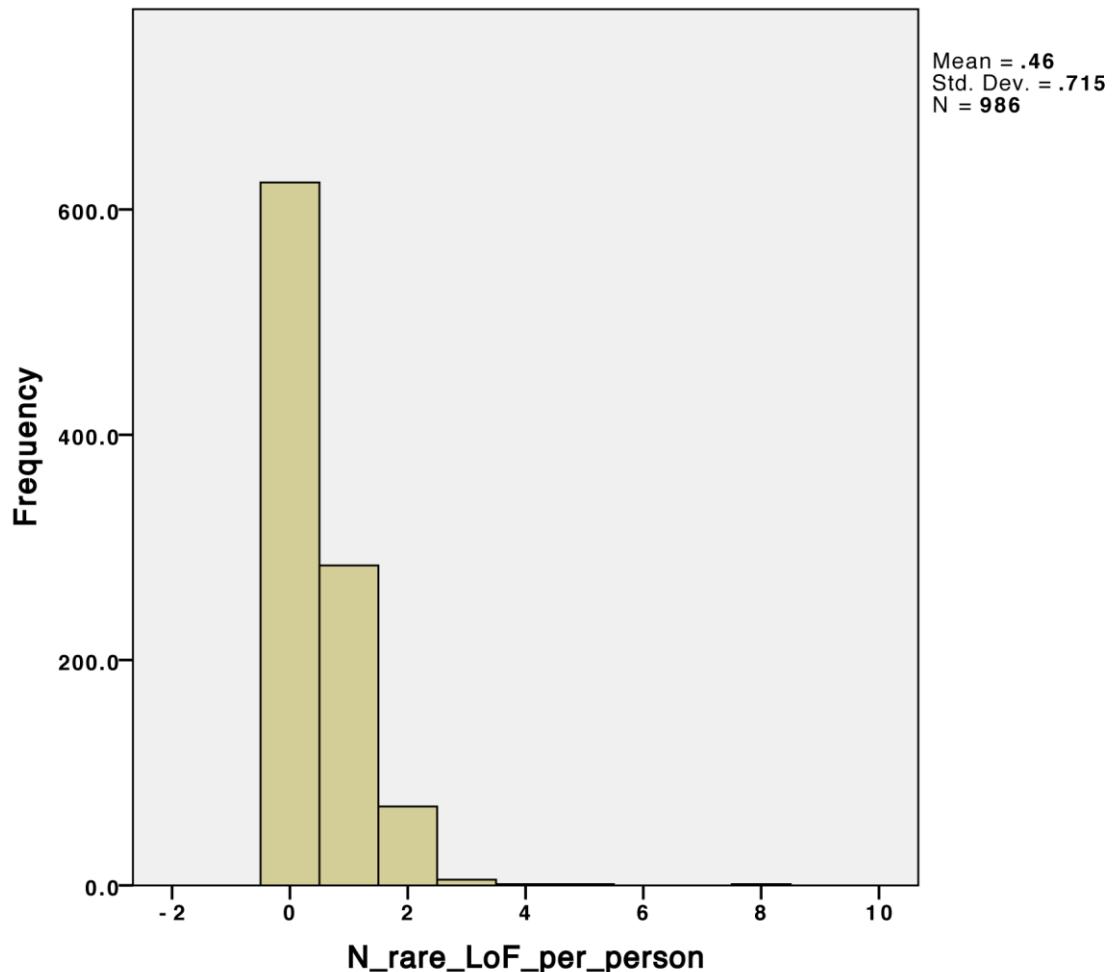
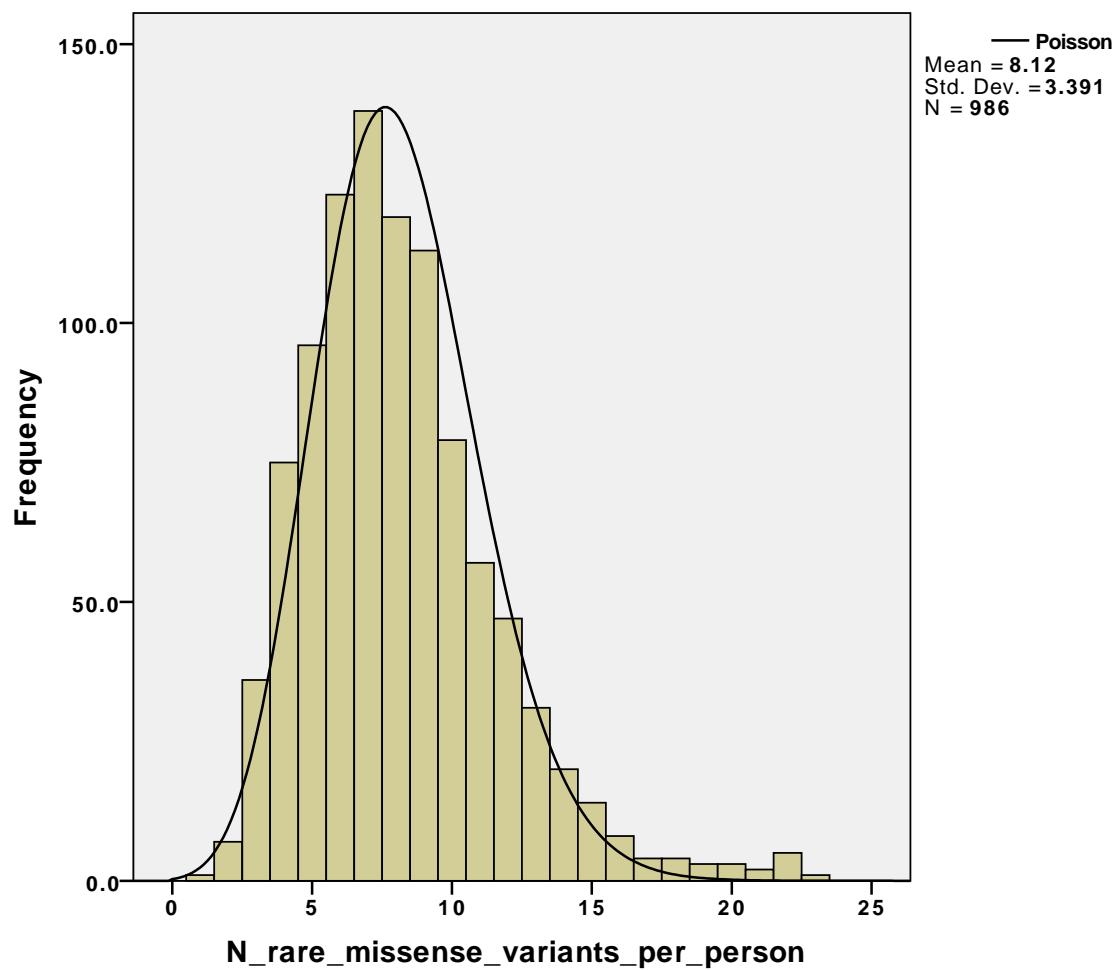


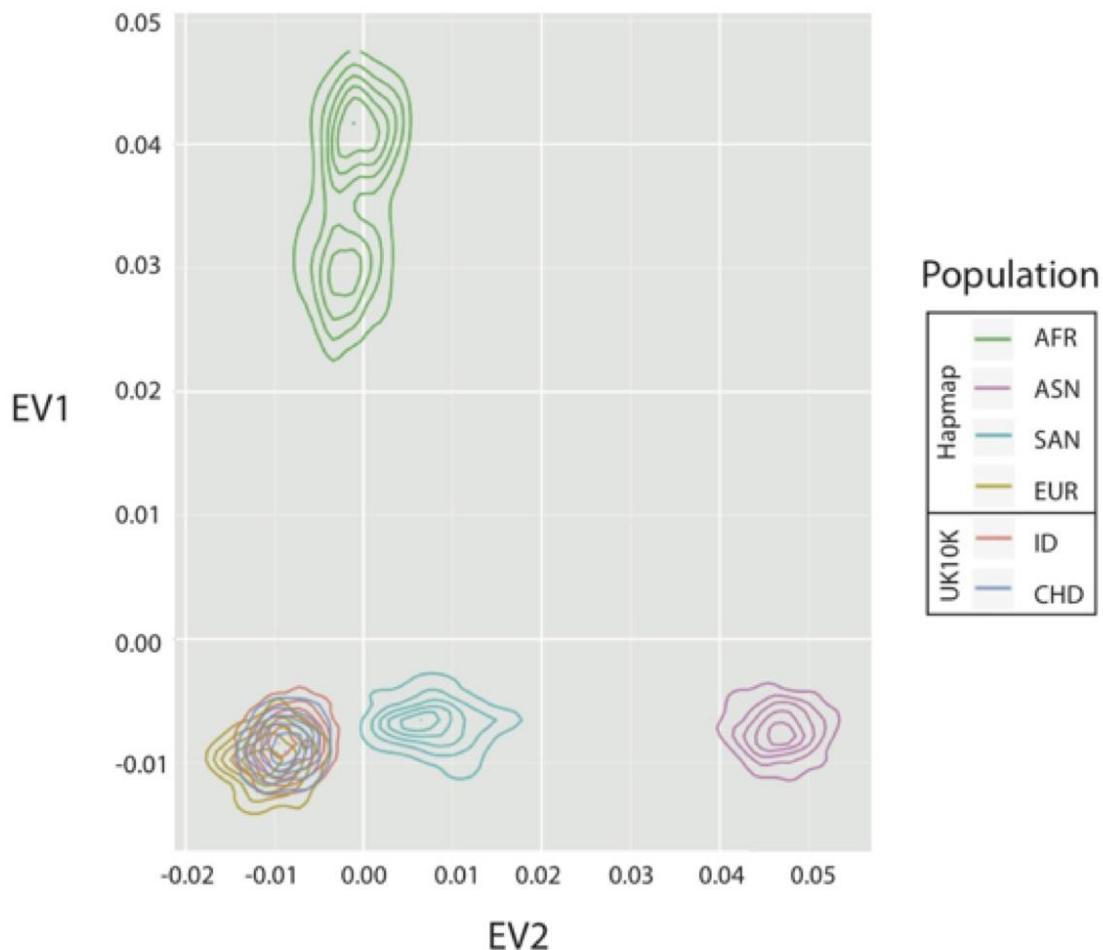
Supp. Figure S1. Variants per person. All variants with MAF<1% taken into account.
N- number



Supp. Figure S2. LoF variants per person. Samples with >30 variants were excluded.
N- number



Supp. Figure S3. Missense variants per person. Samples with >30 variants were excluded.
N- number



Supp. Figure S4. Principal component analysis. The first two eigenvectors (EVs) cluster the Hapmap3.3 samples into their component populations (AFR = individuals of African ancestry; ASN = individuals of East Asian ancestry; SAN = individuals of South Asian ancestry; EUR = individuals of European ancestry) [Altshuler et al., 2010]. There is no qualitative difference in population structure between the ID and CHD cohorts.

Supp. Table S1. List sequenced genes

Chromosome	Gene ID	Known or a Candidate Gene	Origin
1	<i>AP4B1</i>	Known	in-house curation
2	<i>KIF5C</i>	Known	in-house curation
3	<i>SETD5</i>	Known	in-house curation
9	<i>MAN1B1</i>	Known	in-house curation
14	<i>AP4S1</i>	Known	in-house curation
15	<i>AP4E1</i>	Known	in-house curation
X	<i>MAOA</i>	Known	in-house curation
X	<i>ARHGEF6</i>	Known	in-house curation
X	<i>ACSL4</i>	Known	in-house curation
X	<i>USP9X</i>	Known	in-house curation
1	<i>PARP1</i>	Known	Gilissen et al. 2014
1	<i>SLC26A9</i>	Known	Gilissen et al. 2014
2	<i>MBD5</i>	Known	Gilissen et al. 2014
2	<i>MYT1L</i>	Known	Gilissen et al. 2014
2	<i>NRXN1</i>	Known	Gilissen et al. 2014
2	<i>MLL3</i>	Known	Gilissen et al. 2014
3	<i>SRGAP3</i>	Known	Gilissen et al. 2014
3	<i>MLH1</i>	Known	Gilissen et al. 2014
5	<i>NSUN2</i>	Known	Gilissen et al. 2014
8	<i>KCNQ3</i>	Known	Gilissen et al. 2014
8	<i>ZFHX4</i>	Known	Gilissen et al. 2014
9	<i>KANK1</i>	Known	Gilissen et al. 2014
9	<i>SPTAN1</i>	Known	Gilissen et al. 2014
10	<i>ANK3</i>	Known	Gilissen et al. 2014
11	<i>SHANK2</i>	Known	Gilissen et al. 2014
12	<i>LRP1</i>	Known	Gilissen et al. 2014
12	<i>SOX5</i>	Known	Gilissen et al. 2014
14	<i>DYNC1H1</i>	Known	Gilissen et al. 2014
16	<i>TBC1D24</i>	Known	Gilissen et al. 2014
17	<i>SMARCE1</i>	Known	Gilissen et al. 2014
19	<i>SMARCA4</i>	Known	Gilissen et al. 2014
20	<i>ARFGEF2</i>	Known	Gilissen et al. 2014
22	<i>SHANK3</i>	Known	Gilissen et al. 2014
X	<i>NLGN4X</i>	Known	Gilissen et al. 2014
X	<i>AGTR2</i>	Known	Gilissen et al. 2014
X	<i>ARHGEF9</i>	Known	Gilissen et al. 2014
X	<i>SHROOM4</i>	Known	Gilissen et al. 2014
X	<i>ZNF41</i>	Known	Gilissen et al. 2014
X	<i>ZNF674</i>	Known	Gilissen et al. 2014
X	<i>SMS</i>	Known	Gilissen et al. 2014
X	<i>CCDC22</i>	Known	Gilissen et al. 2014
X	<i>SYN1</i>	Known	Gilissen et al. 2014
1	<i>SLC2A1</i>	Known	DDG2P list, Gilissen et al. 2014
1	<i>ADCK3</i>	Known	DDG2P list, Gilissen et al. 2014
1	<i>ALG6</i>	Known	DDG2P list, Gilissen et al. 2014
1	<i>ARID1A</i>	Known	DDG2P list, Gilissen et al. 2014
1	<i>GJC2</i>	Known	DDG2P list, Gilissen et al. 2014
2	<i>SATB2</i>	Known	DDG2P list, Gilissen et al. 2014
2	<i>SCN2A</i>	Known	DDG2P list, Gilissen et al. 2014
2	<i>HDAC4</i>	Known	DDG2P list, Gilissen et al. 2014
2	<i>LRP2</i>	Known	DDG2P list, Gilissen et al. 2014

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Chromosome	Gene ID	Known or a Candidate Gene	Origin
2	<i>MMADHC</i>	Known	DDG2P list, Gilissen et al. 2014
2	<i>RAB3GAP1</i>	Known	DDG2P list, Gilissen et al. 2014
2	<i>SOS1</i>	Known	DDG2P list, Gilissen et al. 2014
2	<i>ZEB2</i>	Known	DDG2P list, Gilissen et al. 2014
3	<i>FOXP1</i>	Known	DDG2P list, Gilissen et al. 2014
3	<i>RAF1</i>	Known	DDG2P list, Gilissen et al. 2014
3	<i>CTNNB1</i>	Known	DDG2P list, Gilissen et al. 2014
3	<i>ALG3</i>	Known	DDG2P list, Gilissen et al. 2014
4	<i>AGA</i>	Known	DDG2P list, Gilissen et al. 2014
4	<i>CC2D2A</i>	Known	DDG2P list, Gilissen et al. 2014
4	<i>IDUA</i>	Known	DDG2P list, Gilissen et al. 2014
4	<i>MMAA</i>	Known	DDG2P list, Gilissen et al. 2014
5	<i>MEF2C</i>	Known	DDG2P list, Gilissen et al. 2014
5	<i>NSD1</i>	Known	DDG2P list, Gilissen et al. 2014
6	<i>SYNE1</i>	Known	DDG2P list, Gilissen et al. 2014
6	<i>ARID1B</i>	Known	DDG2P list, Gilissen et al. 2014
6	<i>ALDH5A1</i>	Known	DDG2P list, Gilissen et al. 2014
6	<i>NEU1</i>	Known	DDG2P list, Gilissen et al. 2014
6	<i>SYNGAP1</i>	Known	DDG2P list, Gilissen et al. 2014
6	<i>TUBB2B</i>	Known	DDG2P list, Gilissen et al. 2014
7	<i>CNTNAP2</i>	Known	DDG2P list, Gilissen et al. 2014
7	<i>BRAF</i>	Known	DDG2P list, Gilissen et al. 2014
7	<i>CEP41</i>	Known	DDG2P list, Gilissen et al. 2014
8	<i>CHD7</i>	Known	DDG2P list, Gilissen et al. 2014
8	<i>TRAPPC9</i>	Known	DDG2P list, Gilissen et al. 2014
8	<i>TUSC3</i>	Known	DDG2P list, Gilissen et al. 2014
8	<i>VPS13B</i>	Known	DDG2P list, Gilissen et al. 2014
9	<i>EHMT1</i>	Known	DDG2P list, Gilissen et al. 2014
9	<i>AUH</i>	Known	DDG2P list, Gilissen et al. 2014
9	<i>EXOSC3</i>	Known	DDG2P list, Gilissen et al. 2014
9	<i>FKTN</i>	Known	DDG2P list, Gilissen et al. 2014
9	<i>INPP5E</i>	Known	DDG2P list, Gilissen et al. 2014
9	<i>SMARCA2</i>	Known	DDG2P list, Gilissen et al. 2014
9	<i>STXBP1</i>	Known	DDG2P list, Gilissen et al. 2014
9	<i>TSC1</i>	Known	DDG2P list, Gilissen et al. 2014
9	<i>VLDLR</i>	Known	DDG2P list, Gilissen et al. 2014
10	<i>PTEN</i>	Known	DDG2P list, Gilissen et al. 2014
10	<i>KAT6B</i>	Known	DDG2P list, Gilissen et al. 2014
10	<i>ALDH18A1</i>	Known	DDG2P list, Gilissen et al. 2014
10	<i>ERCC6</i>	Known	DDG2P list, Gilissen et al. 2014
10	<i>POLR3A</i>	Known	DDG2P list, Gilissen et al. 2014
10	<i>SHOC2</i>	Known	DDG2P list, Gilissen et al. 2014
10	<i>WDR11</i>	Known	DDG2P list, Gilissen et al. 2014
11	<i>PAX6</i>	Known	DDG2P list, Gilissen et al. 2014
11	<i>MLL2</i>	Known	DDG2P list, Gilissen et al. 2014
11	<i>DHCR7</i>	Known	DDG2P list, Gilissen et al. 2014
11	<i>HRAS</i>	Known	DDG2P list, Gilissen et al. 2014
11	<i>KIRREL3</i>	Known	DDG2P list, Gilissen et al. 2014
11	<i>PC</i>	Known	DDG2P list, Gilissen et al. 2014
12	<i>SCN8A</i>	Known	DDG2P list, Gilissen et al. 2014
12	<i>GRIN2B</i>	Known	DDG2P list, Gilissen et al. 2014
12	<i>KRAS</i>	Known	DDG2P list, Gilissen et al. 2014
12	<i>POLR3B</i>	Known	DDG2P list, Gilissen et al. 2014

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Chromosome	Gene ID	Known or a Candidate Gene	Origin
12	<i>PTPN11</i>	Known	DDG2P list, Gilissen et al. 2014
12	<i>TUBA1A</i>	Known	DDG2P list, Gilissen et al. 2014
14	<i>FOXG1</i>	Known	DDG2P list, Gilissen et al. 2014
14	<i>GCH1</i>	Known	DDG2P list, Gilissen et al. 2014
14	<i>ZFYVE26</i>	Known	DDG2P list, Gilissen et al. 2014
15	<i>MAP2K1</i>	Known	DDG2P list, Gilissen et al. 2014
15	<i>UBE3A</i>	Known	DDG2P list, Gilissen et al. 2014
15	<i>CHD2</i>	Known	DDG2P list, Gilissen et al. 2014
15	<i>KIF7</i>	Known	DDG2P list, Gilissen et al. 2014
15	<i>SLC12A6</i>	Known	DDG2P list, Gilissen et al. 2014
15	<i>SPRED1</i>	Known	DDG2P list, Gilissen et al. 2014
15	<i>UBR1</i>	Known	DDG2P list, Gilissen et al. 2014
16	<i>CREBBP</i>	Known	DDG2P list, Gilissen et al. 2014
16	<i>ALG1</i>	Known	DDG2P list, Gilissen et al. 2014
16	<i>CDH15</i>	Known	DDG2P list, Gilissen et al. 2014
16	<i>GPR56</i>	Known	DDG2P list, Gilissen et al. 2014
16	<i>GRIN2A</i>	Known	DDG2P list, Gilissen et al. 2014
16	<i>MLYCD</i>	Known	DDG2P list, Gilissen et al. 2014
16	<i>NDE1</i>	Known	DDG2P list, Gilissen et al. 2014
16	<i>TAT</i>	Known	DDG2P list, Gilissen et al. 2014
16	<i>TSC2</i>	Known	DDG2P list, Gilissen et al. 2014
17	<i>KANSL1</i>	Known	DDG2P list, Gilissen et al. 2014
17	<i>NF1</i>	Known	DDG2P list, Gilissen et al. 2014
17	<i>PAFAH1B1</i>	Known	DDG2P list, Gilissen et al. 2014
17	<i>RAI1</i>	Known	DDG2P list, Gilissen et al. 2014
18	<i>SETBP1</i>	Known	DDG2P list, Gilissen et al. 2014
18	<i>TCF4</i>	Known	DDG2P list, Gilissen et al. 2014
19	<i>FKRP</i>	Known	DDG2P list, Gilissen et al. 2014
19	<i>MAP2K2</i>	Known	DDG2P list, Gilissen et al. 2014
19	<i>NFIX</i>	Known	DDG2P list, Gilissen et al. 2014
19	<i>PEPD</i>	Known	DDG2P list, Gilissen et al. 2014
19	<i>PNKP</i>	Known	DDG2P list, Gilissen et al. 2014
19	<i>WDR62</i>	Known	DDG2P list, Gilissen et al. 2014
20	<i>ASXL1</i>	Known	DDG2P list, Gilissen et al. 2014
20	<i>DNMT3B</i>	Known	DDG2P list, Gilissen et al. 2014
21	<i>DYRK1A</i>	Known	DDG2P list, Gilissen et al. 2014
21	<i>PCNT</i>	Known	DDG2P list, Gilissen et al. 2014
22	<i>ADSL</i>	Known	DDG2P list, Gilissen et al. 2014
22	<i>ALG12</i>	Known	DDG2P list, Gilissen et al. 2014
22	<i>EP300</i>	Known	DDG2P list, Gilissen et al. 2014
22	<i>SMARCB1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>ABCD1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>FMR1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>GK</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>TIMM8A</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>AFF2</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>GPC3</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>KDM5C</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>OFD1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PTCHD1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>SMC1A</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>TSPAN7</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>OPHN1</i>	Known	DDG2P list, Gilissen et al. 2014

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Chromosome	Gene ID	Known or a Candidate Gene	Origin
X	<i>SLC9A6</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>UPF3B</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>ZDHHC9</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>IL1RAPL1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>ATRX</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>CUL4B</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>AP1S2</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>ARX</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>ATP7A</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>BCOR</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>CASK</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>CDKL5</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>DCX</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>DKC1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>DLG3</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>DMD</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>FGD1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>FLNA</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>FTSJ1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>GDI1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>GRIA3</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>HCCS</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>HCFC1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>HDAC8</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>HPRT1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>HSD17B10</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>HUWE1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>IDS</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>IKBKG</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>IQSEC2</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>L1CAM</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>LAMP2</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>MECP2</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>MED12</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>MID1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>NDP</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>NHS</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>NSDHL</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>OCRL</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>OTC</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PAK3</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PCDH19</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PDHA1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PGK1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PHF6</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PHF8</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PLP1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PORCN</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>PRPS1</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>RPS6KA3</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>SHOX</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>SLC16A2</i>	Known	DDG2P list, Gilissen et al. 2014
X	<i>SLC6A8</i>	Known	DDG2P list, Gilissen et al. 2014

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X	SOX3	Known	DDG2P list, Gilissen et al. 2014
X	SYP	Known	DDG2P list, Gilissen et al. 2014
X	UBE2A	Known	DDG2P list, Gilissen et al. 2014
1	ALDH4A1	Known	DDG2P list
1	DDOST	Known	DDG2P list
1	PPT1	Known	DDG2P list
2	KIF1A	Known	DDG2P list
3	ACY1	Known	DDG2P list
3	GLB1	Known	DDG2P list
4	PRSS12	Known	DDG2P list
5	GM2A	Known	DDG2P list
5	HEXB	Known	DDG2P list
5	OXCT1	Known	DDG2P list
6	GRIK2	Known	DDG2P list
6	ARG1	Known	DDG2P list
6	RNASET2	Known	DDG2P list
8	CA8	Known	DDG2P list
8	HGSNAT	Known	DDG2P list
11	DEAF1	Known	DDG2P list
11	ALG8	Known	DDG2P list
11	ATM	Known	DDG2P list
11	CTSD	Known	DDG2P list
12	PAH	Known	DDG2P list
12	MMAB	Known	DDG2P list
15	HEXA	Known	DDG2P list
15	SPG11	Known	DDG2P list
16	PRRT2	Known	DDG2P list
17	COX10	Known	DDG2P list
17	SGSH	Known	DDG2P list
17	TSEN54	Known	DDG2P list
19	CC2D1A	Known	DDG2P list
19	FTL	Known	DDG2P list
19	GCDH	Known	DDG2P list
22	MLC1	Known	DDG2P list
22	TUBA8	Known	DDG2P list
X	BRWD3	Known	DDG2P list
X	PQBP1	Known	DDG2P list
X	NDUFA1	Known	DDG2P list
X	RAB39B	Known	DDG2P list
X	ZNF711	Known	DDG2P list
X	FAM58A	Known	DDG2P list
X	IGSF1	Known	DDG2P list
X	TM4SF2	Known	DDG2P list
1	ASH1L	candidate gene	
1	ZMYM6	candidate gene	
1	ACBD6	candidate gene	
1	CNKS1R1	candidate gene	
1	GATAD2B	candidate gene	
1	GON4L	candidate gene	
1	HIST3H3	candidate gene	
1	MTF1	candidate gene	
1	RGS7	candidate gene	
1	ZBTB40	candidate gene	

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Chromosome	Gene ID	Known or a Candidate Gene	Origin
1	<i>ST3GAL3</i>	candidate gene	
1	<i>KDM1A</i>	candidate gene	
1	<i>CAP1</i>	candidate gene	
1	<i>KCNH1</i>	candidate gene	
1	<i>ZNF238</i>	candidate gene	
1	<i>NR1I3</i>	candidate gene	
1	<i>BDP1</i>	candidate gene	
1	<i>CCDC23</i>	candidate gene	
1	<i>KIF26B</i>	candidate gene	
1	<i>KLHL21</i>	candidate gene	
1	<i>ODF2L</i>	candidate gene	
1	<i>SLC6A17</i>	candidate gene	
1	<i>ZMYND12</i>	candidate gene	
2	<i>ADRA2B</i>	candidate gene	
2	<i>EEF1B2</i>	candidate gene	
2	<i>GAD1</i>	candidate gene	
2	<i>PECR</i>	candidate gene	
2	<i>GRB14</i>	candidate gene	
2	<i>KCNK12</i>	candidate gene	
2	<i>HSPD1</i>	candidate gene	
2	<i>CAPN10</i>	candidate gene	
2	<i>INPP4A</i>	candidate gene	
2	<i>ARHGEF4</i>	candidate gene	
2	<i>ITGA4</i>	candidate gene	
3	<i>CHL1</i>	candidate gene	
3	<i>DLG1</i>	candidate gene	
3	<i>GTPBP8</i>	candidate gene	
3	<i>PBRM1</i>	candidate gene	
3	<i>SLC6A1</i>	candidate gene	
3	<i>STAG1</i>	candidate gene	
3	<i>TSEN2</i>	candidate gene	
3	<i>ACTL6A</i>	candidate gene	
3	<i>DHX30</i>	candidate gene	
3	<i>SMARCC1</i>	candidate gene	
4	<i>LARP7</i>	candidate gene	
4	<i>PRMT10</i>	candidate gene	
4	<i>AIMP1</i>	candidate gene	
4	<i>GRIA2</i>	candidate gene	
4	<i>CCNA2</i>	candidate gene	
4	<i>DCHS2</i>	candidate gene	
4	<i>PCDH10</i>	candidate gene	
5	<i>NDST1</i>	candidate gene	
5	<i>TRIO</i>	candidate gene	
5	<i>COL4A3BP</i>	candidate gene	
5	<i>GRIA1</i>	candidate gene	
5	<i>CAMK2A</i>	candidate gene	
6	<i>PHIP</i>	candidate gene	
6	<i>ASCC3</i>	candidate gene	
6	<i>MED23</i>	candidate gene	
6	<i>HIVEP2</i>	candidate gene	
6	<i>PHACTR1</i>	candidate gene	
6	<i>PPP2R5D</i>	candidate gene	
6	<i>SYNCRIP</i>	candidate gene	

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Chromosome	Gene ID	Known or a Candidate Gene	Origin
6	<i>HIST1H4B</i>	candidate gene	
6	<i>PHF10</i>	candidate gene	
6	<i>FKBPL</i>	candidate gene	
6	<i>TCP10L2</i>	candidate gene	
6	<i>TENM1</i>	candidate gene	
7	<i>CASP2</i>	candidate gene	
7	<i>CTTNBP2</i>	candidate gene	
7	<i>AP4M1</i>	candidate gene	
7	<i>ACTL6B</i>	candidate gene	
7	<i>LHFPL3</i>	candidate gene	
7	<i>LIMK1</i>	candidate gene	
7	<i>MYO1G</i>	candidate gene	
7	<i>SMARCD3</i>	candidate gene	
7	<i>ZNF425</i>	candidate gene	
8	<i>ERLIN2</i>	candidate gene	
8	<i>TAF2</i>	candidate gene	
8	<i>TTI2</i>	candidate gene	
8	<i>THAP1</i>	candidate gene	
8	<i>CYP7B1</i>	candidate gene	
8	<i>EPPK1</i>	candidate gene	
8	<i>SNTG1</i>	candidate gene	
9	<i>RALGDS</i>	candidate gene	
9	<i>SLC31A1</i>	candidate gene	
9	<i>RAPGEF1</i>	candidate gene	
9	<i>RABL6</i>	candidate gene	
10	<i>WAC</i>	candidate gene	
10	<i>ADK</i>	candidate gene	
10	<i>ENTPD1</i>	candidate gene	
10	<i>CAMK2G</i>	candidate gene	
10	<i>TNKS2</i>	candidate gene	
10	<i>TUBAL3</i>	candidate gene	
11	<i>TMEM135</i>	candidate gene	
11	<i>MED17</i>	candidate gene	
11	<i>SLC25A22</i>	candidate gene	
11	<i>OR5M1</i>	candidate gene	
11	<i>ARL14EP</i>	candidate gene	
11	<i>NRXN2</i>	candidate gene	
11	<i>DLG2</i>	candidate gene	
11	<i>DPF2</i>	candidate gene	
11	<i>NTM</i>	candidate gene	
12	<i>ASCL1</i>	candidate gene	
12	<i>C12orf57</i>	candidate gene	
12	<i>COQ5</i>	candidate gene	
12	<i>KDM5A</i>	candidate gene	
12	<i>ZCCHC8</i>	candidate gene	
12	<i>CUX2</i>	candidate gene	
12	<i>SMARCC2</i>	candidate gene	
12	<i>ARID2</i>	candidate gene	
12	<i>SMARCD1</i>	candidate gene	
12	<i>STAB2</i>	candidate gene	
12	<i>SYT1</i>	candidate gene	
13	<i>FRY</i>	candidate gene	
13	<i>DGKH</i>	candidate gene	

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Chromosome	Gene ID	Known or a Candidate Gene	Origin
13	<i>CDK8</i>	candidate gene	
13	<i>SETDB2</i>	candidate gene	
14	<i>UBR7</i>	candidate gene	
14	<i>YY1</i>	candidate gene	
14	<i>PROX2</i>	candidate gene	
14	<i>ZC3H14</i>	candidate gene	
14	<i>SPTLC2</i>	candidate gene	
14	<i>VRK1</i>	candidate gene	
14	<i>ACIN1</i>	candidate gene	
14	<i>DPF3</i>	candidate gene	
14	<i>PTPN21</i>	candidate gene	
15	<i>LINS</i>	candidate gene	
15	<i>ARIH1</i>	candidate gene	
15	<i>SCAPER</i>	candidate gene	
15	<i>LRRK1</i>	candidate gene	
16	<i>NECAB2</i>	candidate gene	
16	<i>THUMPD1</i>	candidate gene	
17	<i>CACNA1G</i>	candidate gene	
17	<i>FASN</i>	candidate gene	
17	<i>KDM6B</i>	candidate gene	
17	<i>DLG4</i>	candidate gene	
17	<i>TANC2</i>	candidate gene	
17	<i>UBTF</i>	candidate gene	
17	<i>WDR45L</i>	candidate gene	
17	<i>ENTHD2</i>	candidate gene	
17	<i>MGAT5B</i>	candidate gene	
17	<i>MYO1D</i>	candidate gene	
17	<i>SMARCD2</i>	candidate gene	
17	<i>TMEM132E</i>	candidate gene	
18	<i>ELP2</i>	candidate gene	
18	<i>LAMA1</i>	candidate gene	
18	<i>PIGN</i>	candidate gene	
18	<i>MIB1</i>	candidate gene	
18	<i>PIK3C3</i>	candidate gene	
19	<i>TRMT1</i>	candidate gene	
19	<i>ZNF526</i>	candidate gene	
19	<i>TNPO2</i>	candidate gene	
19	<i>KCNC3</i>	candidate gene	
19	<i>SHANK1</i>	candidate gene	
19	<i>TSEN34</i>	candidate gene	
19	<i>DPF1</i>	candidate gene	
20	<i>EEF1A2</i>	candidate gene	
20	<i>PSMA7</i>	candidate gene	
21	<i>IFNAR2</i>	candidate gene	
22	<i>PLA2G6</i>	candidate gene	
22	<i>SREBF2</i>	candidate gene	
X	<i>KIAA2022</i>	candidate gene	
X	<i>MAGT1</i>	candidate gene	
X	<i>NXF5</i>	candidate gene	
X	<i>ZDHHC15</i>	candidate gene	
X	<i>ZMYM3</i>	candidate gene	
X	<i>GSPT2</i>	candidate gene	
X	<i>NAA10</i>	candidate gene	

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Chromosome	Gene ID	Known or a Candidate Gene	Origin
X	<i>RBM10</i>	candidate gene	
X	<i>SRPX2</i>	candidate gene	
X	<i>BCORL1</i>	candidate gene	
X	<i>CLIC2</i>	candidate gene	
X	<i>CNKS2R</i>	candidate gene	
X	<i>DDX3X</i>	candidate gene	
X	<i>EIF2C1</i>	candidate gene	
X	<i>EIF2S3</i>	candidate gene	
X	<i>ELK1</i>	candidate gene	
X	<i>FAAH2</i>	candidate gene	
X	<i>FRMPD4</i>	candidate gene	
X	<i>PGRMC1</i>	candidate gene	
X	<i>RAB40AL</i>	candidate gene	
X	<i>TAF1</i>	candidate gene	
X	<i>TAF7L</i>	candidate gene	
X	<i>THOC2</i>	candidate gene	
X	<i>TMLHE</i>	candidate gene	
X	<i>WDR13</i>	candidate gene	
X	<i>ZCCHC12</i>	candidate gene	
X	<i>ZNF81</i>	candidate gene	
X	<i>ALG13</i>	candidate gene	
X	<i>MAOB</i>	candidate gene	
X	<i>NLGN3</i>	candidate gene	
X	<i>FAM120C</i>	candidate gene	
X	<i>SYTL5</i>	candidate gene	
X	<i>WNK3</i>	candidate gene	
X	<i>ACE2</i>	candidate gene	
X	<i>ACOT9</i>	candidate gene	
X	<i>AKAP17A</i>	candidate gene	
X	<i>AKAP4</i>	candidate gene	
X	<i>ARHGAP36</i>	candidate gene	
X	<i>ARHGAP6</i>	candidate gene	
X	<i>ARSF</i>	candidate gene	
X	<i>ASB12</i>	candidate gene	
X	<i>ASMT</i>	candidate gene	
X	<i>ASMTL</i>	candidate gene	
X	<i>ATP2B3</i>	candidate gene	
X	<i>ATXN3L</i>	candidate gene	
X	<i>AVPR2</i>	candidate gene	
X	<i>AWAT2</i>	candidate gene	
X	<i>BMP15</i>	candidate gene	
X	<i>BTK</i>	candidate gene	
X	<i>CACNA1F</i>	candidate gene	
X	<i>CCNB3</i>	candidate gene	
X	<i>CD99</i>	candidate gene	
X	<i>CDK16</i>	candidate gene	
X	<i>CFP</i>	candidate gene	
X	<i>CLCN4</i>	candidate gene	
X	<i>CLCN5</i>	candidate gene	
X	<i>CMC4</i>	candidate gene	
X	<i>COL4A6</i>	candidate gene	
X	<i>CPXCR1</i>	candidate gene	
X	<i>CRLF2</i>	candidate gene	

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Chromosome	Gene ID	Known or a Candidate Gene	Origin
X	<i>CSF2RA</i>	candidate gene	
X	<i>CSTF2</i>	candidate gene	
X	<i>CTPS2</i>	candidate gene	
X	<i>CXORF22</i>	candidate gene	
X	<i>CXORF58</i>	candidate gene	
X	<i>DDX26B</i>	candidate gene	
X	<i>DDX53</i>	candidate gene	
X	<i>DHRSX</i>	candidate gene	
X	<i>DIAPH2</i>	candidate gene	
X	<i>DOCK11</i>	candidate gene	
X	<i>ENOX2</i>	candidate gene	
X	<i>ESX1</i>	candidate gene	
X	<i>FAM47B</i>	candidate gene	
X	<i>GAB3</i>	candidate gene	
X	<i>GABRQ</i>	candidate gene	
X	<i>GLRA2</i>	candidate gene	
X	<i>GPR112</i>	candidate gene	
X	<i>GPRASP1</i>	candidate gene	
X	<i>HAUS7</i>	candidate gene	
X	<i>HDHD1</i>	candidate gene	
X	<i>HS6ST2</i>	candidate gene	
X	<i>IL3RA</i>	candidate gene	
X	<i>ITIH6</i>	candidate gene	
X	<i>KCND1</i>	candidate gene	
X	<i>KIF4A</i>	candidate gene	
X	<i>KLHL15</i>	candidate gene	
X	<i>KLHL34</i>	candidate gene	
X	<i>KLHL4</i>	candidate gene	
X	<i>LAS1L</i>	candidate gene	
X	<i>MAGEA11</i>	candidate gene	
X	<i>MAGEB1</i>	candidate gene	
X	<i>MAGEB10</i>	candidate gene	
X	<i>MAGEB2</i>	candidate gene	
X	<i>MAGEC1</i>	candidate gene	
X	<i>MAGEC3</i>	candidate gene	
X	<i>MAGED1</i>	candidate gene	
X	<i>MAGEE2</i>	candidate gene	
X	<i>MAGIX</i>	candidate gene	
X	<i>MAP3K15</i>	candidate gene	
X	<i>MAP7D3</i>	candidate gene	
X	<i>MBNL3</i>	candidate gene	
X	<i>MORC4</i>	candidate gene	
X	<i>MSL3</i>	candidate gene	
X	<i>MTMR1</i>	candidate gene	
X	<i>MTMR8</i>	candidate gene	
X	<i>MXRA5</i>	candidate gene	
X	<i>NA</i>	candidate gene	
X	<i>NKAP</i>	candidate gene	
X	<i>NRK</i>	candidate gene	
X	<i>NXF4</i>	candidate gene	
X	<i>OGT</i>	candidate gene	
X	<i>P2RY4</i>	candidate gene	
X	<i>P2RY8</i>	candidate gene	

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Chromosome	Gene ID	Known or a Candidate Gene	Origin
X	<i>PABPC5</i>	candidate gene	
X	<i>PASD1</i>	candidate gene	
X	<i>PHKA1</i>	candidate gene	
X	<i>PIN4</i>	candidate gene	
X	<i>PJA1</i>	candidate gene	
X	<i>PLCXD1</i>	candidate gene	
X	<i>PLXNB3</i>	candidate gene	
X	<i>POLA1</i>	candidate gene	
X	<i>PRDX4</i>	candidate gene	
X	<i>PRICKLE3</i>	candidate gene	
X	<i>PRRG1</i>	candidate gene	
X	<i>PRRG3</i>	candidate gene	
X	<i>PSMD10</i>	candidate gene	
X	<i>RENBP</i>	candidate gene	
X	<i>RGAG1</i>	candidate gene	
X	<i>RGN</i>	candidate gene	
X	<i>RLIM</i>	candidate gene	
X	<i>RPGR</i>	candidate gene	
X	<i>SHROOM2</i>	candidate gene	
X	<i>SLC25A53</i>	candidate gene	
X	<i>SLC25A6</i>	candidate gene	
X	<i>SPRY3</i>	candidate gene	
X	<i>STARD8</i>	candidate gene	
X	<i>SYTL4</i>	candidate gene	
X	<i>TBC1D8B</i>	candidate gene	
X	<i>TCEAL3</i>	candidate gene	
X	<i>TKTL1</i>	candidate gene	
X	<i>TLR8</i>	candidate gene	
X	<i>TREX2</i>	candidate gene	
X	<i>TSC22D3</i>	candidate gene	
X	<i>USP27X</i>	candidate gene	
X	<i>UTP14A</i>	candidate gene	
X	<i>VAMP7</i>	candidate gene	
X	<i>WWC3</i>	candidate gene	
X	<i>XIAP</i>	candidate gene	
X	<i>XKRX</i>	candidate gene	
X	<i>ZFX</i>	candidate gene	

References for the DDG2P list- [The Deciphering Developmental Disorders Study, 2014]; Gilissen et al. 2014- [Gilissen et al., 2014].

Supp. Table S2. All rare, coding SNPs and indels identified in this study, including non-pathogenic variants

These data are based on the GRCh37/hg19 version of the reference genome. The variants pass quality control and variant frequency metrics as explained in the Materials and Methods and Results sections. Functional annotations were added with the Ensembl Variant Effect Predictor 2.8 against Ensembl 70, and, where the variant affects multiple transcripts, the most severe consequence is reported here, which is not necessarily the canonical gene transcript corresponding to the GenBank mRNA NCBI Reference Sequence. Most of these variants are of unknown significance/likely not to be pathogenic. The likely pathogenic variants, inferred based on the criteria described in the Materials and Methods and the Results sections of the article are in Supp. Tables S3 and S4, as well as in this table. GERP- Genomic Evolutionary Rate Profiling conservation score [Cooper et al., 2005]; Polyphen- tool for annotating coding nonsynonymous SNPs [Adzhubei et al., 2010]; SIFT- tool for predicting whether an amino acid substitution affects protein function [Kumar et al., 2009]; Condel- CONsensus DELetiousness score of non-synonymous single nucleotide variants [Clifford et al., 2004]; Sample ID- Unique identifier of the studied individuals.

Supp. Table S2 is available as a separate Excel file under the Supporting Information for this article.

Supp. Table S3. Likely causative LoF variants

Chromosome	Genomic DNA Position (hg19 coordinates)	Reference Allele	Alternate allele	Genotype	Effect Variant	NCBI rsID	Gene	Ensembl Transcript	HGVSc Coding DNA Variant Description (Generated with Mutalyzer 2.0.8)	HGVSp Protein Variant Description (Generated with Mutalyzer 2.0.8)	Position in Coding Sequence	Amino Acid Position	HGMD	Pathogenicity Assessment	Frequency in ExAC data [Number of alleles with the alternate variant/how many individuals in total]	Frequency in NHLBI Exome Variant Server	Sample ID	Gender
1	155408842	G	A	G/A	stop_gained		ASH1L	ENST00000392403	NM_018489.2(ASH1L_001);c.510C>T	NM_018489.2(ASH1L_001);p.(Arg1702*)	5104	1702		candidate, in Table 4 main text	0	0	UK10K_FINDWG5411302	male
X	54099713	G	A	A/A	stop_gained		FAM120C	ENST0000328235	XM_005262021.1(FAM120C_001);c.2632C>T	XM_005262021.1(FAM120C_001);p.(Gln878*)	2632	878		candidate, in Table 4 main text	0	0	UK10K_FINDWG5410866	male
6	17010331	C	T	C/T	splice_donor_variant		PHF10	ENST0000339209	NM_018288.3;c.1113+1G>A		0	0		candidate, in Table 4 main text	0	0	UK10K_FINDWG5411045	male
6	170119016	T	G	T/G	splice_acceptor_variant		PHF10	ENST0000339209	NM_018288.3;c.195-2A>C		0	0		candidate, in Table 4 main text	0	0	UK10K_FINDWG5411632	male
6	78727244	CA	C	C/A/C	frameshift_variant		PHIP	ENST0000275034	NM_017934.5(PHIP_001);c.1050del	NM_017934.5(PHIP_001);p.(Phe350Leufs*32)	1050-1051	350-351		candidate, in Table 4 main text	0	0	UK10K_FINDWG5411669	male
19	13226256	G	GA	G/GA	frameshift_variant		TRMT1	ENST0000221504	NM_001142554.1(TRMT1_001);c.477_478insA	NM_001142554.1(TRMT1_001);p.(Leu160Thrfs*42)	477-478	159-160		candidate, in Table 4 main text	0	0	UK10K_FINDWG5410941	male
19	13226262	C	CA	C/C/A	frameshift_variant		TRMT1	ENST0000221504	NM_001142554.1(TRMT1_001);c.471_472insA	NM_001142554.1(TRMT1_001);p.(Glu158Argfs*44)	471-472	157-158		candidate, in Table 4 main text	0	0	UK10K_FINDWG5410941	male
10	28884798	CA	C	C/A/C	frameshift_variant		WAC	ENST0000354911	NM_016628.4(WAC_001);c.148del	NM_016628.4(WAC_001);p.(Ile250Serfs*81)	748	250		candidate, in Table 4 main text	0	0	UK10K_FINDWG5410715	male
X	54343454	C	T	T/T	splice_donor_variant		WNK3	ENST0000354646	NM_020922.3(c.1089+1G>A)		0	0		candidate, in Table 4 main text	0	0	UK10K_FINDWG5410823	male
1	35453525	A	T	A/T	stop_gained		ZMYM6	ENST0000357182	NM_007167.3(ZMYM6_001);c.3158T>A	NM_007167.3(ZMYM6_001);p.(Leu1053*)	3158	1053		candidate, in Table 4 main text	0	0	UK10K_FINDWG5411034	male
1	35453525	A	T	A/T	stop_gained		ZMYM6	ENST0000357182	NM_007167.3(ZMYM6_001);c.3158T>A	NM_007167.3(ZMYM6_001);p.(Leu1053*)	3158	1053		candidate, in Table 4 main text	0	0	UK10K_FINDWG5410504	male
X	108902601	G	A	A/A	stop_gained		ACSL4	ENST0000340800	NM_022977.2(ACSL4_001);c.1960C>T	NM_022977.2(ACSL4_001);p.(Arg654*)	1960	654		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411400	male
X	148049184	C	T	T/T	stop_gained		AFF2	ENST0000286437	NM_00170628.1(AFF2_001);c.2152C>T	NM_00170628.1(AFF2_001);p.(Gln178*)	2152	718		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411410	male
4	178359093	C	T	T/T	stop_gained		AGA	ENST0000264598	NM_000273.3(AGA_001);c.503G>A	NM_000273.3(AGA_001);p.(Trp168*)	503	168	Aspartylglucosaminuria	likely pathogenic, in Table 1 main text	1/16078	0	UK10K_FINDWG5411606	male
6	15754310	C	G	C/G	stop_gained		ARID1B	ENST0000350024	NM_017519.2(ARID1B_001);c.2481G>C	NM_017519.2(ARID1B_001);p.(Tyw28*)	2481	827		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5410663	male
6	157520190	C	T	C/T	stop_gained		ARID1B	ENST0000350026	NM_017519.2(ARID1B_001);c.2152C>T	NM_017519.2(ARID1B_001);p.(Arg1062*)	3184	1062	Coffin-Siris syndrome	likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411529	male
6	157495156	GC	G	GC/G	frameshift_variant		ARID1B	ENST0000340685	NM_020732.3(ARID1B_001);c.304del	NM_020732.3(ARID1B_001);p.(Ala104Glufs*3)	3040-3041	1014		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411501	male
6	157527816	T	TC	T/T/C	frameshift_variant		ARID1B	ENST0000350024	NM_017519.2(ARID1B_001);c.550delup	NM_017519.2(ARID1B_001);p.(Arg138lyst*)	550*	1838		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411495	male
20	31021130	C	T	C/T	stop_gained		ASXL1	ENST0000375687	NM_015338.5(ASXL1_001);c.1129C>T	NM_015338.5(ASXL1_001);p.(Gln37*)	1129	377		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411037	female
X	76953099	TG	T	T/T	frameshift_variant		ATRX	ENST0000395603	NM_138270.2(ATRX_001);c.213del	NM_138270.2(ATRX_001);p.(Lys72Serfs*15)	96	32		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411056	male
X	76972632	G	A	A/A	stop_gained	rs122445108	ATRX	ENST0000373344	NM_000489.4(ATRX_001);c.109C>T	NM_000489.4(ATRX_001);p.(Arg37*)	109	37	ATRX syndrome	likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411171	male
X	76972632	G	A	A/A	stop_gained	rs122445108	ATRX	ENST0000373344	NM_000489.4(ATRX_001);c.109C>T	NM_000489.4(ATRX_001);p.(Arg37*)	109	37	ATRX syndrome	likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5410920	male
X	7677768	I	C	C/C	splice_acceptor_variant		ATRX	ENST0000373344	NM_000489.4(ATRX_001);c.6850A>G		0	0		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411357	male
X	76954083	C	CAT	CAT/CAT	frameshift_variant		ATRX	ENST0000373344	NM_000489.4(ATRX_001);c.166_167dup	NM_000489.4(ATRX_001);p.(Met56Ilefs*)	166-167	56		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411068	male
X	76972632	G	A	A/A	stop_gained	rs122445108	ATRX	ENST0000373344	NM_000489.4(ATRX_001);c.109C>T	NM_000489.4(ATRX_001);p.(Arg37*)	109	37	ATRX syndrome	likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411170	male
X	7999648	A	T	T/T	stop_gained		BRWD3	ENST0000373275	NM_153252.4(BRWD3_001);c.696T>A	NM_153252.4(BRWD3_001);p.(Ter132*)	696	232		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5410888	male
X	79845282	AC	A	A/A	frameshift_variant		BRWD3	ENST0000373275	NM_153252.4(BRWD3_001);c.379del1	NM_153252.4(BRWD3_001);p.(Ser1264lefs*13)	3791	1264		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5410935	male
8	61714153	G	T	G/T	splice_donor_variant		CHD7	ENST0000423902	NM_017780.3(c.2442+1G>T)		0	0		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411365	male
8	61763879	G	T	G/T	splice_donor_variant		CHD7	ENST0000423902	NM_017780.3(c.5665+1G>T)		0	0		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411541	male
3	4162750	GC	G	G/GC	frameshift_variant		CTNNB1	ENST0000340498	NM_001904.3(CTNNB1_001);c.835del	NM_001904.3(CTNNB1_001);p.(Leu29Qysfs*26)	835	279		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5410768	male
3	41275708	C	T	C/T	stop_gained		CTNNB1	ENST0000340498	NM_001904.3(CTNNB1_001);c.1603C>T	NM_001904.3(CTNNB1_001);p.(Arg53*)	1603	535		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411300	male
X	119680444	T	TA	TA/TA	frameshift_variant		CUL4B	ENST0000371322	NM_001079872.1(CUL4B_001);c.803dup	NM_001079872.1(CUL4B_001);p.(Leu268Phefs*5)	803	268		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5410985	male
X	119668443	T	C	C/C	splice_acceptor_variant		CUL4B	ENST0000371322	NM_001079872.1(c.2161-2A>G)		0	0		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411353	male
X	119675604	G	A	A/A	stop_gained		CUL4B	ENST0000371322	NM_001079872.1(CUL4B_001);c.1396C>T	NM_001079872.1(CUL4B_001);p.(Arg466*)	1396	466		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5410803	male
X	119694060	A	T	T/T	stop_gained		CUL4B	ENST0000371322	NM_001079872.1(CUL4B_001);c.434T>A	NM_001079872.1(CUL4B_001);p.(Leu145*)	434	145		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411451	male
X	119675472	C	T	T/T	stop_gained		CUL4B	ENST0000371322	NM_001079872.1(CUL4B_001);c.1428G>A	NM_001079872.1(CUL4B_001);p.(Ter176*)	1428	476		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411038	male
9	140707923	GTC	G	GTC/G	frameshift_variant		EHMT1	ENST0000460843	NM_024757.4(EHMT1_001);c.3126_3127del	NM_024757.4(EHMT1_001);p.(Gln1043Glufs*133)	3126-3127	1043		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411373	male
3	7105212	T	C	T/C	splice_acceptor_variant		FOXP1	ENST0000316789	NM_0014810.1:c.975-2C>	NM_0014810.1:c.975-2C>	0	0		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411548	male
X	132826445	AC	A	A/A	frameshift_variant		GPC3	ENST0000370818	NM_004484.3(GPC3_001);c.1243del	NM_004484.3(GPC3_001);p.(Val415Trpfs*27)	1243	415		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411558	male
12	1390612	G	A	G/A	stop_gained		GRIN2B	ENST0000279598	NM_000834.3(GRIN2B_001);c.649C>T	NM_000834.3(GRIN2B_001);p.(Gln217*)	649	217		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411446	male
12	13828175	CA	C	C/A/C	frameshift_variant		GRIN2B	ENST0000279598	NM_000834.3(GRIN2B_001);c.1086del	NM_000834.3(GRIN2B_001);p.(Val436Glyfs*2)	1088	363		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411556	male
15	72674903	G	A	G/A	stop_gained	rs121907962	HEXA	ENST0000268097	NM_000520.4(HEXA_001);c.409C>T	NM_000520.4(HEXA_001);p.(Arg137*)	409	137	Tay-Sachs disease	likely pathogenic, in Table 1 main text	2/12858	0	UK10K_FINDWG5411084	male
8	43002207	G	A	A/A	splice_donor_variant		HGSNAT	ENST0000379644	NM_152419.2.c.234A>G		0	0	Mucopolysaccharidosis IIIIC	likely pathogenic, in Table 1 main text	3/11635 (none homozygous)	0	UK10K_FINDWG5411534	female
X	29935691	C	T	T/T	stop_gained		IL1RAPL1	ENST0000379993	NM_014271.3(IL1RAPL1_001);c.889C>T	NM_014271.3(IL1RAPL1_001);p.(Arg297*)	889	297		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG54110964	male
X	29471326	C	CT	CT/CT	frameshift_variant		IL1RAPL1	ENST0000379993	NM_014271.3(IL1RAPL1_001);c.606dup	NM_014271.3(IL1RAPL1_001);p.(Leu237Terfs*8)	606*	203		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411107	male
X	29301120	C	T	T/T	stop_gained		IL1RAPL1	ENST0000379993	NM_014271.3(IL1RAPL1_001);c.148C>T	NM_014271.3(IL1RAPL1_001);p.(Arg50*)	148	50		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG54110971	male
9	745218	C	T	C/T	stop_gained		KANK1	ENST0000382297	NM_015158.3(KANK1_001);c.148C>T	NM_015158.3(KANK1_001);p.(Arg134*)	4042	1348		likely pathogenic, in Table 1 main text	2/12962	0	UK10K_FINDWG54110746	male
9	713465	G	A	G/A	splice_donor_variant		KANK1	ENST0000382293	NM_001256876.1:c.269A>G		0	0		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411454	male
10	76729776	A	G	A/G	splice_acceptor_variant		KAT6B	ENST0000287239	NM_012330.3(KAT6B_001);c.304C>T	NM_012330.3(KAT6B_001);p.(Arg1002*)	3004	1002		likely pathogenic, in Table 1 main text	0	0	UK10K_FINDWG5411456	male
X	53240810	C	A	A/A	stop_gained		KDM6C	ENST0000452825	NM_001146702.1(KDM6C_001);c.1069G>T	NM_001146702.1(KDM6C_001);p.(Glu357*)	1069	357						

Supp. Table S3. Likely causative LoF variants cont.

Chromosome	Genomic DNA Position (hg19 coordinates)	Reference Allele	Alternate allele	Genotype	Effect variant	NCBI rsID	Gene	Ensembl Transcript	HGVSc Coding DNA Variant Description (Generated with Mutalyzer 2.0.8)	HGVSp protein variant description (generated with Mutalyzer 2.0.8)	Position in coding sequence	Amino acid position	HGMD	Pathogenicity assessment	Frequency in ExAC data [Number alleles with the alternate variant/how many individuals in total]	Frequency NHLBI Exome Variant Server	Sample ID	Gender
X	23411323	CTA	C	C/C	frameshift_variant		PTCHD1	ENST00000379361	NM_173495.2(PTCHD1_001);p.(Ile564Argfs*6)	NM_173495.2(PTCHD1_001);p.(Ile564Argfs*6)	1689-1690	563-564		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA541026	male
10	89717672	C	T	C/T	stop_gained	rs121909219	PTEN	ENST00000371953	NM_000314.6(PTEN_001);c.697C>T	NM_000314.6(PTEN_001);p.(Arg233*)	697	233	Cowden disease	likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA541153	male
2	166198965	C	T	C/T	stop_gained		SCN2A	ENST00000283252	NM_021067.2(SCN2A_001);c.2548C>T	NM_021067.2(SCN2A_001);p.(Arg680*)	2548	850		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410774	male
2	166179616	A	T	A/T	stop_gained		SCN2A	ENST00000283252	NM_021067.2(SCN2A_001);c.1822A>T	NM_021067.2(SCN2A_001);p.(Arg608*)	1822	608		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA541069	male
12	52156446	C	T	C/T	stop_gained		SCN8A	ENST00000354534	NM_001177984.2(SCN8A_001);c.2530C>T	NM_001177984.2(SCN8A_001);p.(Arg844*)	2530	844		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411661	male
18	42531178	C	T	C/T	stop_gained		SETBP1	ENST00000282030	NM_015592.2(SETBP1_001);c.1873C>T	NM_015592.2(SETBP1_001);p.(Arg625*)	1873	625		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411268	male
3	9486739	A	T	A/T	stop_gained		SETD5	ENST00000402198	NM_001080517.1(SETD5_001);c.1195A>T	NM_001080517.1(SETD5_001);p.(lys399*)	1195	399		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411029	male
3	9517301	CT	C	CT/C	frameshift_variant		SETD5	ENST00000402198	NM_001080517.1(SETD5_001);c.3856del	NM_001080517.1(SETD5_001);p.(Ser1286Leufs*84)	3856	1286		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410795	male
3	9486877	C	T	C/T	stop_gained		SETD5	ENST00000402198	NM_001080517.1(SETD5_001);c.1333C>T	NM_001080517.1(SETD5_001);p.(Arg445*)	1333	445		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411659	male
3	9517216	A	AG	A/G	frameshift_variant		SETD5	ENST00000402198	NM_001080517.1(SETD5_001);c.3771dup	NM_001080517.1(SETD5_001);p.(Ser1258Glufs*65)	3771	1258		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411248	male
3	9512419	C	T	C/T	stop_gained		SETD5	ENST00000402198	NM_001080517.1(SETD5_001);c.3001C>T	NM_001080517.1(SETD5_001);p.(Arg1001*)	3001	1001		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411283	male
3	9489453	C	G	C/G	stop_gained		SETD5	ENST00000402198	NM_001080517.1(SETD5_001);c.1866C>G	NM_001080517.1(SETD5_001);p.(Tyr622*)	1866	622		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410802	male
3	9490142	TCA	T	TCAT	frameshift_variant		SETD5	ENST00000402198	NM_001080517.1(SETD5_001);c.2177_2178del	NM_001080517.1(SETD5_001);p.(Thr26Asnfs*39)	2177-2178	726		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410830	male
11	70332413	G	A	G/A	stop_gained		SHANK2	ENST00000449833	NM_133265.3(SHANK2_001);c.2221C>T	NM_133265.3(SHANK2_001);p.(Gln741*)	2221	741		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411435	male
X	135106576	TTG	T	T/T	frameshift_variant		SLC9A6	ENST00000370698	NM_001042537.1(SLC9A6_001);c.1554_1555del	NM_001042537.1(SLC9A6_001);p.(Phe520Tyrf*23)	1554-1555	520		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411275	male
X	135081128	G	A	A/A	splice_donor_variant		SLC9A6	ENST00000370695	NM_001042537.1(c.793+1G>A)		0	0		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410836	male
18	52946888	C	T	C/T	splice_acceptor_variant		TCF4	ENST00000354452	NM_001083962.1(TCF4_001);c.550-1G>A		0	0	Pitt-Hopkins syndrome	likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411380	male
18	53017634	G	A	G/A	stop_gained		TCF4	ENST00000354452	NM_001083962.1(TCF4_001);c.505C>T	NM_001083962.1(TCF4_001);p.(Gln169*)	505	169		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410771	male
X	38525419	T	TA	TA/T	frameshift_variant		TSPAN7	ENST00000378482	NM_004615.3(TSPAN7_001);c.127dup	NM_004615.3(TSPAN7_001);p.(Trp43Asnfs*42)	127	43		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410923	male
15	25601177	TA	T	TA/T	frameshift_variant		UBE3A	ENST00000232165	NM_000462.3(UBE3A_001);c.1995del	NM_000462.3(UBE3A_001);p.(Leu665Profs*12)	1995	665		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411225	male
X	118985742	G	GA	GA/GA	frameshift_variant		UPF3B	ENST00000276201	NM_080632.2(UPF3B_001);c.250del	NM_080632.2(UPF3B_001);p.(Ser84Leufs*47)	250-251	84		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410747	male
X	118975080	TTCGT	T	T/T	frameshift_variant		UPF3B	ENST00000276201	NM_080632.2(UPF3B_001);c.762_765del	NM_080632.2(UPF3B_001);p.(Asp254Glufs*8)	762-765	254-255		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411299	male
X	41089847	CA	C	C/C	frameshift_variant		USP9X	ENST00000324545	NM_00103950.2(USP9X_001);c.7574del	NM_00103950.2(USP9X_001);p.(Gln252Argfs*18)	7574	2525		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5411140	male
X	128944967	G	A	A/A	stop_gained		ZDHHC9	ENST00000357166	NM_016032.3(ZDHHC9_001);c.892C>T	NM_016032.3(ZDHHC9_001);p.(Arg298*)	892	298	ID	likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410775	male
X	128945384	G	GA	GA/GA	frameshift_variant		ZDHHC9	ENST00000357166	NM_016032.3(ZDHHC9_001);c.878_879insA	NM_016032.3(ZDHHC9_001);p.(Ser294Glnfs*26)	878-879	293		likely pathogenic, in Table 1 main text	0	0	UK10K_FNDWGA5410704	male

The genomic position of the variants is provided according to the GRCh37/hg19 version of the reference genome; NCBI rsID- reference number if the variant has been annotated in the NCBI dbSNP database; HGVSc Coding DNA Variant Description- the nucleotide numbering uses +1 as the A of the ATG translation initiation codon in the reference sequence, with the initiation codon as codon 1, the description has been generated with Mutalyzer 2.0.8; the HGVSp Protein Variant Description has been generated with Mutalyzer 2.0.8 [Wildeman et al., 2008]; HGMD - annotated if the variant has been observed in the HGMD Professional 2014.3 version [Stenson et al., 2014]; Frequency in ExAC data [Number alleles with the alternate variant/how many individuals in total]- frequency data from the Exome Aggregation Consortium ((ExAC), Cambridge, MA; URL: <http://exac.broadinstitute.org>; accessed November 2014); Frequency NHLBI Exome Variant Server-frequency data from the NHLBI Exome Sequencing Project (Exome Variant Server (EVS), <http://evs.gs.washington.edu/EVS/>) [Tabor et al., 2014]; Sample ID- Unique identifier of the studied individuals.

Supp. Table S4. Likely causative missense variants

Chrom osome	Genomic DNA Position (hg19 coordinates)	Reference Allele	Alternate Allele	Genotype	Effect Variant	NCBI rsID	Gene	Ensembl Transcript	HGVSc Coding DNA Variant Description (Generated with Mutalyzer 2.0.8)	HGVSp Protein Variant Description (Generated with Mutalyzer 2.0.8)	Position in Coding Sequence	Amino Acid Change	HGMd	Pathogenicity Assessment	Frequency in ExAC data (Number alleles with the alternate variant in many individuals in total)	Frequency in NHLBI Exome Variant Server	GERP	PolyPhen	SIFT	Condel	Sample ID	Gender	
6	157431632	G	A	G/A	missense_variant	-	ARID1B	ENST00003046085	NM_020732.3(ARID1B_001).c.2308G>A	NM_020732.3(ARID1B_001).p.(Gly770Arg)	2308	770	R>G	Intellectual disability,plantar-fallopadotarsal syndrome, facial dysmorphisms, botulax exacta, facial variant, (ICCG-)	likely pathogenic,ln Table main Text	0	0	2.17	probably_damaging(0.96)	0	0	UK10K_FNDWGA5410858	male
X	76829787	C	T	T/T	missense_variant	-	ATRX	ENST00003073344	NM_000489.4(ATRX_001).c.6254G>A	NM_000489.4(ATRX_001).p.(Arg208His)	6254	2085	R>H	ATRX syndrome	likely pathogenic,ln Table main Text	0	0	3.84	probably_damaging(0.97)	0	0	UK10K_FNDWGA5411356	male
8	61763644	C	T	C/T	missense_variant	-	CHD7	ENST0000423902	NP_017780.3(CHD7_001).c.558C>T	NP_017780.3(CHD7_001).p.(Pro183Leu)	5588	1863	P>L	CHARGE syndrome	likely pathogenic,ln Table main Text	2/29858	0	3.72	benign(0.021)	tolerated(0.48)	neutral(0.11)	UK10K_FNDWGA5411437	male
7	147964128	G	C	G/C	missense_variant	-	CNTNAP2	ENST0000361727	NP_014145.1(CNTNAP2_001).c.3385G>C	NP_014145.1(CNTNAP2_001).p.(Asp1219His)	3385	1129	D>H	Autism	likely pathogenic,ln Table main Text	2/122966	0	3.48	possibly_damaging(0.883)	deleterious(0.0)	deleterious(0.789)	UK10K_FNDWGA5411520	male
11	7115365	T	C	T/C	missense_variant	-	DHCR7	ENST0000355527	NP_01360.2(DHCR7_001).c.3564G>A	NP_01360.2(DHCR7_001).p.(His119Arg)	3558	119	H>R	Smith-Lemli-Optiz syndrome	likely pathogenic,ln Table main Text	4/11625	0	3.38	probably_damaging(0.946)	deleterious(0.0)	deleterious(0.883)	UK10K_FNDWGA5411429	male
11	71151334	C	T	C/T	missense_variant	-	DHCR7	ENST0000355527	NP_01360.2(DHCR7_001).c.2266G>A	NP_01360.2(DHCR7_001).p.(Val70Ala)	2266	76	V>I	likely pathogenic,ln Table main Text	195/116466	0	1.57	benign(0.006)	tolerated(0.4)	neutral(0.16)	UK10K_FNDWGA5411429	male	
X	325196049	G	A	A/A	missense_variant	r104894791	DMTD	ENST0000357033	NP_000109.3(DMTD_001).p.(Ile102>C)	NP_000109.3(DMTD_001).p.(Ala31Val)	10238	3413	A>V	Muscular dystrophy,Becker	likely pathogenic,ln Table main Text	0	0	2.86	benign(0.04)	tolerated(0.05)	neutral(0.325)	UK10K_FNDWGA5410830	male
X	126216707	G	A	A/A	missense_variant	r137852350	GRIA3	ENST0000264357	NP_000828.4(GRIA3_001).p.(Gly340Asp)	NP_000828.4(GRIA3_001).p.(Gly340Asp)	2497	833	G>R	X-linkedDD	likely pathogenic,ln Table main Text	0	0	4.65	probably_damaging(0.999)	deleterious(0.0)	deleterious(0.935)	UK10K_FNDWGA5411367	male
16	9858474	T	C	T/C	missense_variant	-	GRIN2A	ENST0000303684	NP_001314047.2(GRIN2A_001).c.2972A>G	NP_001314047.2(GRIN2A_001).p.(Asn975Ser)	2972	976	N>S	Epileptic encephalopathy	likely pathogenic,ln Table main Text	0	0	1.96	probably_damaging(0.996)	deleterious(0.0)	deleterious(0.784)	UK10K_FNDWGA5411463	male
11	534289	C	T	C/T	missense_variant	r104894229	HRA5	ENST00004051590	NP_001130442.1(HRA5_001).c.34G>A	NP_001130442.1(HRA5_001).p.(Gly125Ter)	34	12	G>S	Costello syndrome	likely pathogenic,ln Table main Text	0	0	3.15	possibly_damaging(0.525)	deleterious(0.02)	deleterious(0.978)	UK10K_FNDWGA541109	female
8	131392493	G	T	G/T	missense_variant	-	KCNQ3	ENST0000388996	NP_004519.3(KCNQ3_001).p.(His88>C)	NP_004519.3(KCNQ3_001).p.(Arg230Ter)	688	230	R>S	non-syndromicHD	likely pathogenic,ln Table main Text	0	0	5.79	probably_damaging(0.965)	deleterious(0.0)	deleterious(0.851)	UK10K_FNDWGA5410783	male
12	25398279	C	T	C/T	missense_variant	r104894365	KRAS	ENST0000256078	NP_03360.2(KRAS_001).c.406G>A	NP_03360.2(KRAS_001).p.(Val14Ile)	40	14	V>I	Noonan syndrome	likely pathogenic,ln Table main Text	1/10326	0	4.58	probably_damaging(0.977)	deleterious(0.0)	deleterious(0.863)	UK10K_FNDWGA5411395	male
12	25398279	C	T	C/T	missense_variant	r104894365	KRAS	ENST0000256078	NP_03360.2(KRAS_001).c.406G>A	NP_03360.2(KRAS_001).p.(Val14Ile)	40	14	V>I	Noonan syndrome	likely pathogenic,ln Table main Text	1/10326	0	4.58	probably_damaging(0.977)	deleterious(0.0)	deleterious(0.863)	UK10K_FNDWGA5411607	male
15	66721918	A	G	A/G	missense_variant	r121908595	MAP2K1	ENST0000307102	NP_002755.3(MAP2K1_001).c.3894G>T	NP_002755.3(MAP2K1_001).p.(Tyr130Cys)	389	130	Y>C	Cardio-facio-cutaneous syndrome	likely pathogenic,ln Table main Text	0	0	4.02	probably_damaging(0.998)	deleterious(0.0)	deleterious(0.919)	UK10K_FNDWGA5411227	male
X	153929780	G	A	A/A	missense_variant	r161748420	MECP2	ENST0000303391	NP_004992.3(MECP2_001).p.(Arg97>P)	NP_004992.3(MECP2_001).p.(Arg97Ter)	499	167	R>W	Rett syndrome	likely pathogenic,ln Table main Text	0	0	2.8	probably_damaging(0.994)	deleterious(0.0)	deleterious(0.897)	UK10K_FNDWGA5411184	male
X	152936680	G	A	A/A	missense_variant	r182939400	MECP2	ENST0000303391	NP_004992.3(MECP2_001).p.(Ala140Alv)	NP_004992.3(MECP2_001).p.(Ala140Alv)	419	140	A>V	Rett syndrome	likely pathogenic,ln Table main Text	0	0	3.7	probably_damaging(0.97)	deleterious(0.04)	deleterious(0.761)	UK10K_FNDWGA5410713	male
X	152968111	G	C	G/C	missense_variant	r167484048	MECP2	ENST0000303391	NP_004992.3(MECP2_001).p.(Asp156G>C)	NP_004992.3(MECP2_001).p.(Asp156Glu)	468	156	D>E	Rett syndrome	likely pathogenic,ln Table main Text	0	0	3.67	probably_damaging(0.99)	deleterious(0.0)	deleterious(0.886)	UK10K_FNDWGA5411483	female
X	15296725	C	A	A/A	missense_variant	-	MECP2	ENST0000303391	NP_004992.3(MECP2_001).p.(M54G>C)	NP_004992.3(MECP2_001).p.(Gly185Ter)	554	185	G>V	Rett syndrome	likely pathogenic,ln Table main Text	0	0	3.92	probably_damaging(0.998)	deleterious(0.02)	deleterious(0.857)	UK10K_FNDWGA5411185	male
X	15296662	C	G	G/G	missense_variant	r163485860	MECP2	ENST0000303391	NP_004992.3(MECP2_001).p.(G167>C)	NP_004992.3(MECP2_001).p.(Gly206Ala)	617	206	G>A	Rett syndrome	likely pathogenic,ln Table main Text	0	0	3.92	probably_damaging(0.98)	deleterious(0.01)	deleterious(0.845)	UK10K_FNDWGA5410887	male
X	70347217	C	T	T/T	missense_variant	r180338758	MED12	ENST0000336464	NP_05120.2(MED12_001).p.(Val281>C)	NP_05120.2(MED12_001).p.(Arg61Ter)	281	961	R>W	FGS syndrome	likely pathogenic,ln Table main Text	0	0	NA	probably_damaging(0.936)	deleterious(0.01)	deleterious(0.787)	UK10K_FNDWGA5411442	male
X	70347217	C	T	T/T	missense_variant	r180338758	MED12	ENST0000336464	NP_05120.2(MED12_001).p.(Val281>C)	NP_05120.2(MED12_001).p.(Arg61Ter)	281	961	R>W	FGS syndrome	likely pathogenic,ln Table main Text	0	0	NA	probably_damaging(0.936)	deleterious(0.01)	deleterious(0.787)	UK10K_FNDWGA5411178	male
5	176638672	T	G	T/G	missense_variant	-	NSD1	ENST000047982	NP_172349.2(NSD1_001).p.(Asp282Asn)	NP_172349.2(NSD1_001).p.(Leu822Arg)	2465	822	L>R	Autism	likely pathogenic,ln Table main Text	3/122408	0	1.27	probably_damaging(0.73)	deleterious(0.0)	deleterious(0.711)	UK10K_FNDWGA5411386	male
X	110383437	C	T	T/T	missense_variant	r121434612	PAK3	ENST0000262836	NP_001122813.1(PAK3_001).p.(Arg197>C)	NP_001122813.1(PAK3_001).p.(Arg75Ter)	199	67	R>C	Mental retardation syndrome, X-linked	likely pathogenic,ln Table main Text	0	0	4.65	probably_damaging(0.964)	deleterious(0.0)	deleterious(0.851)	UK10K_FNDWGA5410571	male
16	2924904	G	A	A/G	missense_variant	-	PRRT2	ENST0000300797	NP_001256443.1(PRRT2_001).p.(G296A>C)	NP_001256443.1(PRRT2_001).p.(Glu177Ter)	529	177	E>K	Paroxysmal kinesigenic dyskinesia	likely pathogenic,ln Table main Text	0	0	2.85	benign(0.275)	deleterious(0.01)	neutral(0.435)	UK10K_FNDWGA5410887	male
10	89653851	T	C	T/C	missense_variant	-	PTEN	ENST0000371953	NP_000314.6(PTEN_001).p.(Ile50Thr)	NP_000314.6(PTEN_001).p.(Leu50Ter)	149	50	I>T	yes,DM,Macropachyilia	likely pathogenic,ln Table main Text	0	0	3.73	probably_damaging(0.979)	deleterious(0.0)	deleterious(0.867)	UK10K_FNDWGA5411083	male
10	112724120	A	G	A/G	missense_variant	-	SHOC2	ENST0000265277	NP_001269039.1(SHOC2_001).c.4>A	NP_001269039.1(SHOC2_001).p.(Ser26Gly)	4	2	S>G	Noonan-like syndrome with loose skin	likely pathogenic,ln Table main Text	0	0	4.06	probably_damaging(0.925)	deleterious(0.0)	deleterious(0.818)	UK10K_FNDWGA5411252	male
1	43395364	T	A	T/A	missense_variant	r14835799	SLC2A1	ENST0000426263	NP_005616.2(SLC2A1_001).c.767A>T	NP_005616.2(SLC2A1_001).p.(Lys76Met)	767	256	K>M	Glucose transporter deficiency syndrome	likely pathogenic,ln Table main Text	0	0	2.54	probably_damaging(0.98)	deleterious(0.0)	deleterious(0.869)	UK10K_FNDWGA5411443	male
1	43395365	T	C	T/C	missense_variant	r121909738	SLC2A1	ENST0000426263	NP_005616.2(SLC2A1_001).c.727C>T	NP_005616.2(SLC2A1_001).p.(Arg92Ter)	724	92	R>W	Paroxysmal kinesigenic dyskinesia	likely pathogenic,ln Table main Text	0	0	1.34	possibly_damaging(0.811)	deleterious(0.01)	deleterious(0.945)	UK10K_FNDWGA5411443	male
1	43396718	G	A	G/A	missense_variant	-	SLC2A1	ENST0000372500	NP_005616.2(SLC2A1_001).c.766A>G	NP_005616.2(SLC2A1_001).p.(Lys76Glu)	766	256	K>E	Glucose transporter deficiency syndrome	likely pathogenic,ln Table main Text	0	0	2.93	probably_damaging(1)	deleterious(0.0)	deleterious(0.945)	UK10K_FNDWGA5410904	male
X	21985430	G	A	A/A	missense_variant	r121434610	SMS	ENST0000379404	NP_00125842.1(SMS_001).p.(Gly166>C)	NP_00125842.1(SMS_001).p.(Gly166Ter)	166	56	G>S	Snyder-Robinson syndrome	likely pathogenic,ln Table main Text	0	0	4.41	benign(0.132)	tolerated(0.22)	neutral(0.053)	UK10K_FNDWGA5410846	male
9	130447888	C	G	C/G	missense_variant	-	STXBP1	ENST0000373299	NP_001032221.3(STXBP1_001).p.(G165C>G)	NP_001032221.3(STXBP1_001).p.(Arg51Gly)	1651	551	R>G	Autism	likely pathogenic,ln Table main Text	0	0	4.51	probably_damaging(1)	deleterious(0.0)	deleterious(0.945)	UK10K_FNDWGA5411254	male
12	49578884	C	T	C/T	missense_variant	r13783050	TUBA1A	ENST0000295766	NP_001207399.1(TUBA1A_001).p.(Asp422His)	NP_001207399.1(TUBA1A_001).p.(Arg422Ter)	1265	422	R>H	Lissencephaly	likely pathogenic,ln Table main Text	0	0	1.84	benign(0.129)	0	0	UK10K_FNDWGA5410837	male
X	128957700	G	A	A/A	missense_variant	r137852214	ZDHHC9	ENST0000357166	NP_16032.3(ZDHHC9_001).c.442C>T	NP_16032.3(ZDHHC9_001).p.(Arg148Ter)	442	148	R>W	X-linkedDD	likely pathogenic,ln Table main Text	0	0	4.64	probably_damaging(0.998)	deleterious(0.0)	deleterious(0.919)	UK10K_FNDWGA5411590	male
15	72639044	G	A	G/A	missense_variant	HEXA	ENST0000268097	NP_000520.4(HEXA_001).c.1154C>T	NP_000520.4(HEXA_001).p.(Pro385Leu)	1154	385	P>L	likely pathogenic,ln Table main Text	0	0	NA	possibly_damaging(0.488)	deleterious(0.01)	0	UK10K_FNDWGA5411084	male		
														compound heterozygote at the locus	also L0 variant observed Table main Text								
8	43025804	C	A	A/A	missense_variant	HGSNAT	ENST00003079644	NM_12419.2(HGSNAT_001).c.710C>A	NM_12419.2(HGSNAT_001).p.(Pro237Gln)	710	237	P>Q	Mucopolysaccharidosis IIIIC	likely pathogenic,ln Table main Text	1/10280 (1st homozygous)	0	0.25	benign(0.038)	tolerated(0.42)	neutral(0.016)	UK10K_FNDWGA5411534	female	

The genomic position of the variants is provided according to the GRCh37/hg19 version of the reference genome; NCBI rsID- reference number if the variant has been annotated in the NCBI dbSNP database; HGVSc Coding DNA Variant Description- the nucleotide numbering uses +1 as the A of the ATG translation initiation codon in the reference sequence, with the initiation codon as codon 1, the description has been generated with Mutalyzer 2.0.8; the HGVSp Protein Variant Description has been generated with Mutalyzer 2.0.8 [Wildeman et al., 2008]; HGMD- annotated if the variant has been observed in the HGMD Professional 2014.3 version [Stenson et al., 2014]; Frequency in ExAC data [Number alleles with the alternate variant/how many individuals in total]- frequency data from the Exome Aggregation Consortium ((ExAC), Cambridge, MA; URL: <http://exac.broadinstitute.org>; accessed November 2014); Frequency NHLBI Exome Variant Server-frequency data from the NHLBI Exome Sequencing Project (Exome Variant Server (EVS), <http://evs.gs.washington.edu/EVS/>) [Tabor et al., 2014]; GERP- Genomic Evolutionary Rate Profiling conservation score [Cooper et al., 2005]; Polyphen- tool for annotating coding nonsynonymous SNPs [Adzhubei et al., 2010]; SIFT- tool for predicting whether an amino acid substitution affects protein function [Kumar et al., 2009]; Condel- CONsensus DELetiousness score of non-synonymous single nucleotide variants [Clifford et al., 2004]; Sample ID- Unique identifier of the studied individuals.

Supp. Text S1. Consortia Members

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A full list of consortium members can be found at the UK10K Project website (<http://www.uk10k.org>).

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Supp. References

- Adzhubei IA, Schmidt S, Peshkin L, Ramensky VE, Gerasimova A, Bork P, Kondrashov AS, Sunyaev SR. 2010. A method and server for predicting damaging missense mutations. Nat Methods 7:248-249.
- Altshuler DM, Gibbs RA, Peltonen L, Altshuler DM, Gibbs RA, Peltonen L, Dermitzakis E, Schaffner SF, Yu F, Peltonen L, Dermitzakis E, Bonnen PE, et al. 2010. Integrating common and rare genetic variation in diverse human populations. Nature 467:52-58.
- Clifford RJ, Edmonson MN, Nguyen C, Buetow KH. 2004. Large-scale analysis of non-synonymous coding region single nucleotide polymorphisms. Bioinformatics 20:1006-1014.
- Cooper GM, Stone EA, Asimenos G, Green ED, Batzoglou S, Sidow A. 2005. Distribution and intensity of constraint in mammalian genomic sequence. Genome Res 15:901-913.

Supporting Information, Targeted Next Generation Sequencing Analysis of 1000 individuals with Intellectual Disability, Grozeva et al.

- Gilissen C, Hehir-Kwa JY, Thung DT, Van De Vorst M, Van Bon BW, Willemsen MH, Kwint M, Janssen IM, Hoischen A, Schenck A, Leach R, Klein R, et al. 2014. Genome sequencing identifies major causes of severe intellectual disability. *Nature* 511:344-347.
- Kumar P, Henikoff S, Ng PC. 2009. Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. *Nat Protoc* 4:1073-1081.
- Stenson PD, Mort M, Ball EV, Shaw K, Phillips A, Cooper DN. 2014. The Human Gene Mutation Database: building a comprehensive mutation repository for clinical and molecular genetics, diagnostic testing and personalized genomic medicine. *Hum Genet* 133:1-9.
- Tabor HK, Auer PL, Jamal SM, Chong JX, Yu JH, Gordon AS, Graubert TA, O'donnell CJ, Rich SS, Nickerson DA, Bamshad MJ. 2014. Pathogenic variants for mendelian and complex traits in exomes of 6,517 European and african americans: implications for the return of incidental results. *Am J Hum Genet* 95:183-193.
- The Deciphering Developmental Disorders Study. 2014. Large-scale discovery of novel genetic causes of developmental disorders. *Nature* 519:223-228.
- Wildeman M, Van Ophuizen E, Den Dunnen JT, Taschner PE. 2008. Improving sequence variant descriptions in mutation databases and literature using the Mutalyzer sequence variation nomenclature checker. *Hum Mutat* 29:6-13.